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Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see Authors & Referees and the Editorial Policy Checklist.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. figure legend, table legend, main text, or Methods section).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement
☐	☒	An indication of whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
☐	☒	The statistical test(s) used AND whether they are one- or two-sided *Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
☒	☐	A description of all covariates tested
☐	☒	A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
☐	☒	A full description of the statistics including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
☐	☒	For null hypothesis testing, the test statistic (e.g. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P values as exact values whenever suitable.*
☒	☐	For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
☒	☐	For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
☒	☐	Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	Agilent MassHunter Quantitative Analysis software (version B.05.00) was used for quantifying the lipid species measured in the study.
Data analysis	Data analysis was performed using STATA software or GraphPad Prism 7

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.

Data

Policy information about availability of data

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

We have provided Supplementary Dataset 1, 3, 4, 5 for our complete proteomic data, in which UniProt IDs are provided for the proteins detected in the experiments. We have provided Supplementary Dataset 2 for all lifespan data. We have provided Supplementary Tables 3-5 for the abundance of all the lipid species measured in the metabolomics experiments.

Field-specific reporting

Please select the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical analysis was performed to determine sample sizes. The sample sizes in the study were chosen based on prior knowledge on the intrinsic variability of the experiments performed.
Data exclusions	No data were excluded.
Replication	All the experiments were performed at least twice and the trends were reproducible between experiments.
Randomization	Allocation of C. elegans belonging to each strain was randomized.
Blinding	Investigators were not blinded during data collection or analysis. The acquired experimental data are precise measurements of live/dead animals, enzymatic activities, and lipids.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☐	☒ Unique biological materials
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Unique biological materials

Policy information about availability of materials

Obtaining unique materials	OD3609 (△faah-4), VV213 (△y53f4b.18), and VV214(△faah-4;△y53f4b.18) strains are available upon request.

Antibodies

Antibodies used	Anti-Flag Sigma-Aldrich Cat#: F7425; RRID: AB_439687 HRP-labeled anti-mouse Santa Cruz Cat#: SC-2005; RRID: AB_631736 HRP-labeled anti-rabbit Santa Cruz Cat#: SC-2030; RRID: AB_631747 GAPDH Santa Cruz Cat#: SC-32233; RRID: AB_627679
Validation	Antibodies validated by manufacturer and in the following publication: Bar-Peled, L. et al. A Tumor suppressor complex with GAP activity for the Rag GTPases that signal amino acid sufficiency to mTORC1. Science 340, 1100-1106, doi:10.1126/science.1232044 (2013).

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	HEK293T cells were all from ATCC

Authentication	The cell lines used have been authenticated by ATCC
Mycoplasma contamination	All the cell line used were tested and found to be negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines were used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	No laboratory animals were used in this study.
Wild animals	No wild animals were used in this study.
Field-collected samples	No field-collected samples were used in this study.